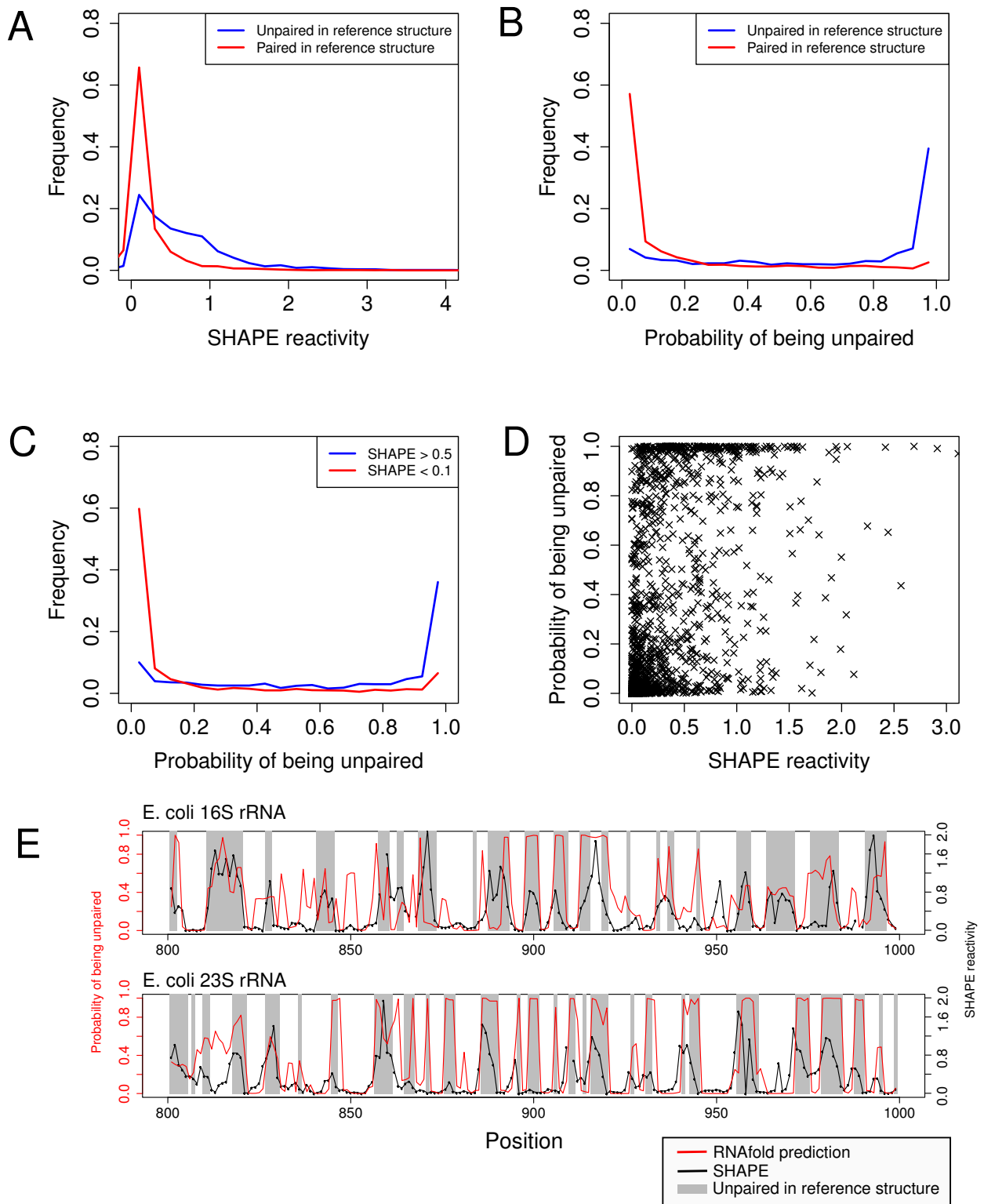


Supplementary Figure 1



(A) Distribution of SHAPE reactivity scores for positions that are paired and unpaired in the reference structure derived from phylogenetic analysis. (B) Distribution of predicted probabilities of being unpaired for positions paired and unpaired in the reference structure. Predictions were made by RNAfold. (C) Distribution of predicted probabilities of being unpaired for positions with high and low SHAPE scores. (D) SHAPE reactivity scores vs. predicted probabilities of being unpaired. (E) Comparison of SHAPE signal, predicted pairing probabilities and reference structure for two 200 nt regions in the 16S and 23S rRNA.